RAW SEQUENCE LISTING   DATE: 01/24/2002
PATENT APPLICATION: US/10/028,051   TIME: 15:04:36

Input Set : N:\Crf3\RULE60\10028051.txt
Output Set: N:\CRF3\01242002\J028051.raw

SEQUENCE LISTING

```
C-->  5 (1) GENERAL INFORMATION:
      7         (i) APPLICANT: Luyten, Frank P.
      8                        Hoang, Bang
      9                        Moos, Jr., Malcolm
     10                        Wang, Shouwen
C--> 12        (ii) TITLE OF INVENTION: ISOLATION AND USE OF TISSUE
     13                               GROWTH INDUCING FRZB PROTEIN
     15       (iii) NUMBER OF SEQUENCES: 23
     17        (iv) CORRESPONDENCE ADDRESS:
     18                 (A) ADDRESSEE: Knobbe, Martens, Olson & Bear
     19                 (B) STREET: 620 Newport Center Drive, 16th Floor
     20                 (C) CITY: Newport Beach
     21                 (D) STATE: CA
     22                 (E) COUNTRY: U.S.A.
     23                 (F) ZIP: 92660
     25         (v) COMPUTER READABLE FORM:
     26                 (A) MEDIUM TYPE: Diskette
     27                 (B) COMPUTER: IBM Compatible
     28                 (C) OPERATING SYSTEM: DOS
     29                 (D) SOFTWARE: FastSEQ Version 1.5
     31        (vi) CURRENT APPLICATION DATA:
C--> 32                 (A) APPLICATION NUMBER: US/10/028,051
C--> 33                 (B) FILING DATE: 19-Dec-2001
     34                 (C) CLASSIFICATION:
     36       (vii) PRIOR APPLICATION DATA:
     37                 (A) APPLICATION NUMBER: 08/729,452
     38                 (B) FILING DATE:
     42      (viii) ATTORNEY/AGENT INFORMATION:
     43                 (A) NAME: Bartfeld, Neil S
     44                 (B) REGISTRATION NUMBER: 39,901
     45                 (C) REFERENCE/DOCKET NUMBER: NIH133.001A
     47        (ix) TELECOMMUNICATION INFORMATION:
     48                 (A) TELEPHONE: 619-235-8550
     49                 (B) TELEFAX: 619-235-0176
     50                 (C) TELEX:
     53 (2) INFORMATION FOR SEQ ID NO: 1:
     55         (i) SEQUENCE CHARACTERISTICS:
     56                 (A) LENGTH: 2374 base pairs
     57                 (B) TYPE: nucleic acid
     58                 (C) STRANDEDNESS: single
     59                 (D) TOPOLOGY: linear
     61        (ix) FEATURE:
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Input Set : N:\Crf3\RULE60\10028051.txt
Output Set: N:\CRF3\01242002\J028051.raw

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63          (A) NAME/KEY: Coding Sequence
64          (B) LOCATION: 256...1230
65          (D) OTHER INFORMATION:
68       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70   AATAGATGCC GCGGCCCCAG AAGTCTTAGA CGTCGGGAAA GAGCAGCCGG AGAGGCAGGG     60
71   GCGGCGGCGG CTGGCGCTCG GCGCAGCTTT TGGGACCCCA TTGAGGGAAT TTGATCCAAG    120
72   GAAGCTGTGA GATTGCCGGG GGAGGAGAAG CTCCCATATC ATTGTGTCCA CTTCCAGGGC    180
73   GGGGAGGAGG AAACGGCGGA GCGGGCCTCT CGGCGTTCTC CGCACTGCTG CACCCTGCCC    240
74   CATCCTGCCG AGATC ATG GTC TGC GGG AGC CGA GGC GGG ATG CTG CTG CTG    291
75                    Met Val Cys Gly Ser Arg Gly Gly Met Leu Leu Leu
76                     1               5                  10
78   CCG GCC GGG CTA CTC GCC CTG GCT GCG CTC TGC CTG CTC CGC GTG CCC    339
79   Pro Ala Gly Leu Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro
80           15                  20                  25
82   GGA GCG CGG GCG GCC GCC TGT GAG CCC GTT CGC ATT CCC CTG TGC AAG    387
83   Gly Ala Arg Ala Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys
84           30                  35                  40
86   TCC CTG CCC TGG AAC ATG ACT AAG ATG CCC AAC CAC CTG CAC CAC AGC    435
87   Ser Leu Pro Trp Asn Met Thr Lys Met Pro Asn His Leu His His Ser
88   45                  50                  55                  60
90   ACC CAG GCC AAC GCC ATC CTG GCC ATC GAG CAG TTC GAA GGT CTG CTG    483
91   Thr Gln Ala Asn Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu
92               65                  70                  75
94   GGC ACC CAC TGC AGC CCG GAT CTG CTC TTC TTC CTC TGT GCT ATG TAC    531
95   Gly Thr His Cys Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr
96               80                  85                  90
98   GCG CCC ATC TGC ACC ATT GAC TTC CAG CAC GAG CCC ATC AAG CCC TGC    579
99   Ala Pro Ile Cys Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys
100              95                 100                 105
102  AAG TCT GTG TGC GAG CGG GCC CGG CAG GGC TGT GAG CCC ATC CTC ATC    627
103  Lys Ser Val Cys Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile
104          110                 115                 120
106  AAG TAC CGC CAC TCG TGG CCG GAA AGC CTG GCC TGC GAG GAG CTG CCA    675
107  Lys Tyr Arg His Ser Trp Pro Glu Ser Leu Ala Cys Glu Glu Leu Pro
108  125                 130                 135                 140
110  GTA TAT GAC CGC GGC GTG TGC ATC TCT CCG GAG GCC ATC GTC ACT GCC    723
111  Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala
112              145                 150                 155
114  GAC GGA GCC GAT TTT CCT ATG GAT TCC AGT AAT GGA AAC TGT AGA GGA    771
115  Asp Gly Ala Asp Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly
116              160                 165                 170
118  GCA AGC AGT GAA CGC TGC AAA TGT AAA CCA GTC AGA GCT ACA CAG AAG    819
119  Ala Ser Ser Glu Arg Cys Lys Cys Lys Pro Val Arg Ala Thr Gln Lys
120              175                 180                 185
122  ACC TAT TTC CGA AAC AAT TAC AAC TAT GTC ATT CGG GCT AAA GTT AAA    867
123  Thr Tyr Phe Arg Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys
124          190                 195                 200
126  GAA ATA AAG ACC AAG TGT CAT GAT GTG ACT GCA GTA GTG GAG GTG AAG    915
127  Glu Ile Lys Thr Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys
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128  205                     210                     215                     220
130  GAG ATT TTA AAG GCT TCT CTG GTA AAC ATT CCA AGG GAA ACT GTG AAC    963
131  Glu Ile Leu Lys Ala Ser Leu Val Asn Ile Pro Arg Glu Thr Val Asn
132              225                     230                     235
134  CTT TAT ACC AGC TCT GGC TGC CTG TGT CCT CCA CTT AAC GTT AAT GAG   1011
135  Leu Tyr Thr Ser Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu
136              240                     245                     250
138  GAG TAT CTC ATC ATG GGC TAC GAA GAT GAA GAG CGC TCC AGA TTA CTG   1059
139  Glu Tyr Leu Ile Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu
140              255                     260                     265
142  TTG GTA GAA GGT TCT ATT GCT GAG AAA TGG AAG GAT CGA CTT GGT AAA   1107
143  Leu Val Glu Gly Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys
144        270                     275                     280
146  AAA GTT AAG CGG TGG GAT ATG AAG CTC CGT CAT CTT GGA CTG AAT ACA   1155
147  Lys Val Lys Arg Trp Asp Met Lys Leu Arg His Leu Gly Leu Asn Thr
148  285                     290                     295                     300
150  AGT GAT TCT AGC CAT AGT GAT TCC ACT CAG AGT CAG AAG CCT GGC AGG   1203
151  Ser Asp Ser Ser His Ser Asp Ser Thr Gln Ser Gln Lys Pro Gly Arg
152              305                     310                     315
154  AAT TCT AAC TCC CGG CAA GCA CGC AAC TAAATCCTGA AATGCAGAAA ATCCTCA  1257
155  Asn Ser Asn Ser Arg Gln Ala Arg Asn
156              320                     325
158  GTGGACTTCC TATTAAGACT TGCATTGCTG GACTAGCAAA GGCAAATTGC ACTATTGCAC  1317
159  GTCATAGTCT ATTTTTTAGC CACAAAAATC AGGTGGTAAC TGATATTACT TCTATTTTTT  1377
160  CTTTTGTTTT CTGCTTTTCT CCTTCCCCCA TTCCCTTTTT TGTGGTCTGA GTACAGATCC  1437
161  TTAAATATAT TATATGTATT CTATTTCACT AATCATGGGA AAACTGTTCT TTGCAATAAT  1497
162  AATAAATTAA ACATGTTGAT ACCAGGGCCT CTTTGCTGGA GTAAATGTTA ATTTGCTGTT  1557
163  CTGCACCCAG ATTGGGAATG CAATATTGGA TGCAAAGAGA GATTTCTGGT ATACAGAGAA  1617
164  AGCTAGATAG GCTGTAAAGC ATACTTTGCT GATCTAATTA CAGCCTCATT CTTGCATGCC  1677
165  TTTTGGCATT CTCCTCACGC TTAGAAAGTT CTAAATGTTT ATAAAGGTAA AATGACAGTT  1737
166  TGAAATCAAA TGCCAACAGG CAGAGCAATC AAGCACCAGG AAGCATTTAT GAAGAAATGA  1797
167  CACATGAGAT GAATTATTTG CAAGATTGGC AGGAAGCAAA ATAAATAGCA TTAGGAGCTG  1857
168  GGGATAGAGC ATTTTGCCTG ACTGAGAAGC ACAACTGAAG CTAGTAGCTG TTGGGGTGTT  1917
169  AACAGCAGCA TTTTTCTTTT GACGATACAT TTGTTTGTCT GTGAATATAT TGATCAGCAT  1977
170  TAGAGCAGTG GATTGTGACC AGACATCAGG TGTTATCAGC ATAGCTCTGT TTAATTTGCT  2037
171  TCCTTTTAGA TGAACGCATT GGTGTCTTTT TTTTCTTCTT TTAAAATAAA TCTCCCTTGC  2097
172  TGCATTTGAC CAGGAAAAGA AAGCATATAT GCATGTGCAC CGGGCTGTTA TTTTTAAGAT  2157
173  ATGTAGCTCT ATAAAACGCT ATAGTCAAAA GATGGTAAAA TGTGCAAGAT CTGGGTGTG   2217
174  TGTATTAATG TGTGTGTGTC CGCATACACT CACACTCAAG CTGAAGTGAA CGACAGGCCT  2277
175  GTGCACTGGC CTGCACTTTA TCATTTGGAT TTGTGCTGTT TAATGCTCAG TAAAATATGC  2337
176  TTAATAAAAG GAAAAAAAAA AAAAAAAAAA AAAAAAA                           2374
178  (2) INFORMATION FOR SEQ ID NO: 2:
180          (i) SEQUENCE CHARACTERISTICS:
181              (A) LENGTH: 325 amino acids
182              (B) TYPE: amino acid
183              (C) STRANDEDNESS: single
184              (D) TOPOLOGY: linear
186         (ii) MOLECULE TYPE: protein
187          (v) FRAGMENT TYPE: internal
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Input Set : N:\Crf3\RULE60\10028051.txt
Output Set: N:\CRF3\01242002\J028051.raw

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189    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
191    Met Val Cys Gly Ser Arg Gly Gly Met Leu Leu Leu Pro Ala Gly Leu
192     1               5                   10                  15
193    Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala
194             20                  25                  30
195    Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
196             35                  40                  45
197    Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
198         50                  55                  60
199    Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
200    65                  70                  75                  80
201    Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
202                 85                  90                  95
203    Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
204                 100                 105                 110
205    Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
206             115                 120                 125
207    Ser Trp Pro Glu Ser Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg
208         130                 135                 140
209    Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
210    145                 150                 155                 160
211    Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu
212                 165                 170                 175
213    Arg Cys Lys Cys Lys Pro Val Arg Ala Thr Gln Lys Thr Tyr Phe Arg
214             180                 185                 190
215    Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr
216             195                 200                 205
217    Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
218         210                 215                 220
219    Ala Ser Leu Val Asn Ile Pro Arg Glu Thr Val Asn Leu Tyr Thr Ser
220    225                 230                 235                 240
221    Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Leu Ile
222                 245                 250                 255
223    Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
224                 260                 265                 270
225    Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
226             275                 280                 285
227    Trp Asp Met Lys Leu Arg His Leu Gly Leu Asn Thr Ser Asp Ser Ser
228         290                 295                 300
229    His Ser Asp Ser Thr Gln Ser Gln Lys Pro Gly Arg Asn Ser Asn Ser
230    305                 310                 315                 320
231    Arg Gln Ala Arg Asn
232                 325
234    (2) INFORMATION FOR SEQ ID NO: 3:
236        (i) SEQUENCE CHARACTERISTICS:
237            (A) LENGTH: 1484 base pairs
238            (B) TYPE: nucleic acid
239            (C) STRANDEDNESS: single
240            (D) TOPOLOGY: linear
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Input Set : N:\Crf3\RULE60\10028051.txt
Output Set: N:\CRF3\01242002\J028051.raw

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242     (ix) FEATURE:
244             (A) NAME/KEY: Coding Sequence
245             (B) LOCATION: 208...1182
246             (D) OTHER INFORMATION:
249     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
251  CGGGGCCTGG GCGGSAGGGG CGGTGGCTGG AGCTCGGTAA AGCTCGTGGG ACCCCATTGG    60
252  GGGAATTTGA TCCAAGGAAG CGGTGATTGC CGGGGGAGGA GAAGCTCCCA GATCCTTGTG   120
253  TCCACTTGCA GCGGGGGAGG CGGAGACGCG GAGCGGGCCT TTTGGCGTCC ACTGCGCGGC   180
254  TGCACCCTGC CCCATCCTGC CGGGATC ATG GTC TGC GGC AGC CCG GGA GGG ATG   234
255                               Met Val Cys Gly Ser Pro Gly Gly Met
256                                1                   5
258  CTG CTG CTG CGG GCC GGG CTG CTT GCC CTG GCT GCT CTC TGC CTG CTC    282
259  Leu Leu Leu Arg Ala Gly Leu Leu Ala Leu Ala Ala Leu Cys Leu Leu
260  10              15                  20                  25
262  CGG GTG CCC GGG GCT CGG GCT GCA GCC TGT GAG CCC GTC CGC ATC CCC    330
263  Arg Val Pro Gly Ala Arg Ala Ala Ala Cys Glu Pro Val Arg Ile Pro
264              30                  35                  40
266  CTG TGC AAG TCC CTG CCC TGG AAC ATG ACT AAG ATG CCC AAC CAC CTG    378
267  Leu Cys Lys Ser Leu Pro Trp Asn Met Thr Lys Met Pro Asn His Leu
268              45                  50                  55
270  CAC CAC AGC ACT CAG GCC AAC GCC ATC CTG GCC ATC GAG CAG TTC GAA    426
271  His His Ser Thr Gln Ala Asn Ala Ile Leu Ala Ile Glu Gln Phe Glu
272              60                  65                  70
274  GGT CTG CTG GGC ACC CAC TGC AGC CCC GAT CTG CTC TTC TTC CTC TGT    474
275  Gly Leu Leu Gly Thr His Cys Ser Pro Asp Leu Leu Phe Phe Leu Cys
276      75                  80                  85
278  GCC ATG TAC GCG CCC ATC TGC ACC ATT GAC TTC CAG CAC GAG CCC ATC    522
279  Ala Met Tyr Ala Pro Ile Cys Thr Ile Asp Phe Gln His Glu Pro Ile
280  90                  95                  100                 105
282  AAG CCC TGT AAG TCT GTG TGC GAG CGG GCC CGG CAG GGC TGT GAG CCC    570
283  Lys Pro Cys Lys Ser Val Cys Glu Arg Ala Arg Gln Gly Cys Glu Pro
284              110                 115                 120
286  ATA CTC ATC AAG TAC CGC CAC TCG TGG CCG GAG AAC CTG GCC TGC GAG    618
287  Ile Leu Ile Lys Tyr Arg His Ser Trp Pro Glu Asn Leu Ala Cys Glu
288              125                 130                 135
290  GAG CTG CCA GTG TAC GAC AGG GGC GTG TGC ATC TCT CCC GAG GCC ATC    666
291  Glu Leu Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile
292              140                 145                 150
294  GTT ACT GCG GAC GGA GCT GAT TTT CCT ATG GAT TCT AGT AAC GGA AAC    714
295  Val Thr Ala Asp Gly Ala Asp Phe Pro Met Asp Ser Ser Asn Gly Asn
296      155                 160                 165
298  TGT AGA GGG GCA AGC AGT GAA CGC TGT AAA TGT AAG CCT ATT AGA GCT    762
299  Cys Arg Gly Ala Ser Ser Glu Arg Cys Lys Cys Lys Pro Ile Arg Ala
300  170                 175                 180                 185
302  ACA CAG AAG ACC TAT TTC CGG AAC AAT TAC AAC TAT GTC ATT CGG GCT    810
303  Thr Gln Lys Thr Tyr Phe Arg Asn Asn Tyr Asn Tyr Val Ile Arg Ala
304              190                 195                 200
306  AAA GTT AAA GAG ATA AAG ACT AAG TGC CAT GAT GTG ACT GCA GTA GTG    858
307  Lys Val Lys Glu Ile Lys Thr Lys Cys His Asp Val Thr Ala Val Val
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Input Set : **N:\Crf3\RULE60\10028051.txt**
Output Set: **N:\CRF3\01242002\J028051.raw**

L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:12 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12